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UNITED STATES PATENT APPLICATION

OF

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FOR

DETECTION OF A GENE, [vatD], vatE ENCODING AN

ACETYLTRANSFERASE INACTIVATING STREPTOGRAMIN

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BACKGROUND OF THE INVENTION

This application claims the right to priority based on Provisional Patent Application No. 60/146,141 filed July 30, 1999. The entire disclosure of Provisional Patent Application No. 60/146,141 is hereby incorporated by reference.

This invention relates to the discovery of a new gene, [vatD] <sup>vatE</sup> encoding an acetyltransferase inactivating streptogramin A, which is widely distributed in virginiamycin-resistant *enterococcus faecium* strains.

Streptogramin, virginiamycin, pristinamycin, and synergistin are produced by streptomyces, and consist of synergistic mixtures of two chemically different molecules: A and B compounds (10). In some European countries and in Algeria, these mixtures are used both orally and topically, mostly against staphylococcal infections. Virginiamycin is used as growth promoter in animal feed in Europe and in the U.S.A. Virginiamycin-resistant *Enterococcus faecium* are prevalent in fecal and intestinal samples from turkeys, pigs, broilers, and farmers in Europe and America (1, 14, 19, 20). Since bacteria can be transferred via food from animals to humans, this is alarming, in particular because quinupristin/dalfopristin (J. Antimicrob. Agents Chemother., 1992, 30[suppl.30]), an injectable mixture of semi-synthetic streptogramins soon to be commercialized (Synercid), is expected to be widely used, mainly to treat vancomycin-resistant *E. faecium* infections.

The *sata* gene (18) encoding an acetyltransferase inactivating A compounds was isolated from an *E. faecium*

5 plasmid. It was found in only 29 % of the 140 tested  
10 *E. faecium* strains isolated in Dutch and Danish farms and  
resistant to the mixtures (13, 14). Five of the *E.*  
*faecium* strains isolated in Denmark harbored a large  
plasmid conferring resistance to the mixture and which  
was transferable by filter mating experiments to an *E.*  
*faecium* recipient (14). None of the transconjugants  
harboring these plasmids carried *satA*, *vat*, *vatB*, *vga*, or  
*vgaB* (14). These results suggested that the *E. faecium*  
strains contained other unidentified streptogramin A  
resistance gene(s). Thus, there continues to exist a  
need in the art for the identification of new genes  
specific for *Enterococcus faecium* resistant to  
streptogramin A and related compounds.

#### SUMMARY OF THE INVENTION

15 Accordingly, this invention aids in fulfilling this  
need in the art by providing a new gene, [*vatD*]<sup>*vatE*</sup> encoding  
an acetyltransferase inactivating Streptogramin A, which  
is widely distributed in virginiamycin-resistant  
20 *Enterococcus faecium* strains. In particular, this  
invention provides a purified peptide-comprising the  
complete amino acid sequence (SEQ ID NO:1) encoded by the  
[*vatD*]<sup>*vatE*</sup> gene. This invention also provides polypeptide  
fragments derived from SEQ ID NO:1 containing at least 10  
25 amino acids. The fragments can be common to all  
virginiamycin A acetyl transferases as shown on SEQ ID  
NOS:5, 6, 7, and 8. The fragments according to the  
invention can be specific of as shown on SEQ ID NOS:9,  
10, 11, and 12.

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This invention additionally provides a purified polynucleotide comprising the complete nucleic acid sequence of the vatE gene (SEQ ID NO:2). This invention also provides nucleic acid fragments derived from SEQ ID NOS:3 and 4 containing 15 to 40 nucleotides as primers F and R. For example, the fragments are those corresponding to nucleotides No. 899 to 878 and to nucleotides No. 354 to nucleotide 378. (Fig. 1)

In addition, two primers have been selected in order to obtain, after using an amplification technique and after cloning the amplified sequence, the complete gene of vatE capable of being expressed in *Staphylococcus aureus* (strain No. 4220 described by KREISWIRTH et al. in Nature 1983, Vol. 306, pp. 709-712]. These primers are shown in SEQ ID NOS:13 and 14 as vatEA and vatEB. The vatEA is from nucleotide 98 to nucleotide 120 (Figure 1). The vatEB is from nucleotide 982 to nucleotide 957 (Figure 1).

In SEQ ID NOS:13 and 14, an artificial site was created if comparing with the original sequence in Figure 1 at nucleotides No. 107 and 109 where G was replaced by T and G was replaced by C, respectively. An EcoRI site was then produced in the first primer. In the same manner, in SEQ ID NOS:3 and 4, at nucleotide No. 362, A replaces G (as in the original sequence) and at nucleotide 367, C replaces G (as in the original sequence). A new EcoRI site was created. In the second primer of SEQ ID NOS:3 and 4, a new EcoRI site was created by replacing at nucleotide No. 891 G by C and on the complementary strand (as shown) the base C (original) is replaced by G.

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This invention also provides a composition comprising purified polynucleotide sequences including at least one nucleotide sequence of the genes selected from the group consisting of synthetic polynucleotides or fragments of genes or cDNA of [*vatD*]<sup>*vatE*</sup> useful for the detection of resistance to streptogramin A and related compounds. The gene [*vatD*]<sup>*vatE*</sup> was obtained from a *Hind*III fragment of 5 kb prepared from *enterococcus faecium* genome (strain K14) after digestion by *Hind*III restriction enzyme. The *Hind* III fragment hybridizes with an amplicon containing two degenerated or consensus primers referred to as M and N, which are defined as SEQ ID NOS:5, 6, 7, and 8. This amplicon has 147 nucleotides. The amplicon or the two degenerated primers (M and N) can be used for the preparation of DNA chips as taught in PCT applications No. W095.11.995 and No. WO 97.02.357. The sequences upstream and downstream of this amplicon were obtained.

The DNA fragment containing the [*vatD*]<sup>*vatE*</sup> gene including the amplicon is shown in Figure 1. A region having in this said fragment, the possible properties of a bacterial promoter activity is located as follows in Figure 1. Its sequence is:

-35  
TGTCACA  
-10

201 ACTACTTATT TTTTACCCA ATCTTCTAGA CTATAAT  
XbaI

(SEQ ID NO:16)

Additionally, the invention includes a purified polynucleotide that hybridizes specifically under

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stringent conditions with a polynucleotide of SEQ ID NOS:  
2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12.

The invention further includes polynucleotide  
fragments comprising at least 10 nucleotides capable of  
5 hybridization under stringent conditions with any one of  
the nucleotide sequences enumerated above.

In another embodiment of the invention, a  
recombinant DNA sequence comprising at least one  
nucleotide sequence enumerated above and under the  
10 control of regulatory elements that regulate the  
expression of resistance to antibiotics of the  
streptogramin family in a defined host is provided. The  
amplified complete gene of [*vatD*]<sup>rat E</sup> including the amplicon  
and the promoter, is shown in SEQ ID NO:15.

15 Furthermore, the invention includes a recombinant  
vector comprising the recombinant DNA sequence noted  
above, wherein the vector comprises the plasmid pIP 1801  
contained in *E. coli*. The recombinant strain has been  
deposited at the collection C.N.C.M. in Paris, France,  
20 under the accession number I-2247 on July 7, 1999.

The invention also includes a recombinant cell host  
comprising a polynucleotide sequence enumerated above or  
the recombinant vector defined above.

25 In still a further embodiment of the invention, a  
method detecting bacterial strains that contain the  
polynucleotide sequences set forth above is provided.

Additionally, the invention includes kits for the  
detection of the presence of bacterial strains that  
contain the polynucleotide sequences set forth above.

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The invention also contemplates antibodies recognizing peptide fragments or polypeptides encoded by the polynucleotide sequences enumerated above.

Still further, the invention provides for a screening <sup>method</sup> [met] for active antibiotics and/or molecules for the treatment of infections due to Gram-positive bacteria, particularly enterococci, based on the detection of activity of these antibiotics and/or molecules on bacteria having the resistance phenotype to streptogramins.

#### BRIEF DESCRIPTION OF THE DRAWINGS

This invention will be more fully described with reference to the drawings in which:

FIGURE 1 discloses the complete nucleotide and amino acid sequences of [vatD] <sup>vatE</sup>. In this Figure are also represented the upstream and downstream regions of the vatD gene.

FIGURE 2 is a comparison between the sequences of [vatD] <sup>vatE</sup> protein and four acetyltransferase enzymes already published.

FIGURE 3 is a restriction map of the insert of 1080 bp contained in the plasmid deposited in *E. coli* at C.N.C.M. I-2247.

#### DETAILED DESCRIPTION OF THE INVENTION

The present invention pertains to polynucleotides derived from *Enterococcus faecium* genes encoding resistance to streptogramin A and chemically related compounds. This invention also relates to the use of the polynucleotides as oligonucleotide primers or probes for

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detecting *Enterococcus faecium* strains that are resistant to streptogramin A and related compounds in a biological sample.

5 In another embodiment, the present invention is directed <sup>to</sup> the full length coding sequences of the *Enterococcus faecium* genes encoding resistance to streptogramin A and to the polypeptides expressed by these full length coding sequences.

10 Further, this invention relates to the use of the expressed polypeptides to produce specific monoclonal or polyclonal antibodies that serve as detection means in order to character any *Enterococcus faecium* strain carrying genes encoding resistance to streptogramin A and chemically related compounds

15 The present invention is also directed to diagnostic method for detecting specific strains of *Enterococcus faecium* expected to be contained in a biological sample. The diagnostic methods use the oligonucleotide probes and primers as well as the antibodies of the invention.

20 More particularly, it has now been determined that bacteria from the *Enterococcus faecium* genus carry a [vatD] <sup>vatE</sup> gene, which confers resistance to streptogramin A. A gene encoding an acetyltransferase inactivating streptogramin A was isolated from an *Enterococcus faecium* strain and sequenced. The gene, designated [vatD] <sup>vatE</sup> encodes  
25 a 23,775 kDa protein exhibiting 48.5 to 59.9 % amino acid identity with four other enzymes with the same activity,

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vat, vatB, vatC, and satA. The calculation of the percentage of identity was made by using the program gap of GCG software (version 9.1). The parameters are chosen as follows:

5           a) for amino acid comparisons:

            gap penalty: 12

            gap extension penalty: 4

            length: the sequence to be compared in SEQ ID NO:1 having 213 amino acids.

10           b) for nucleotide comparisons:

            gap penalty: 50

            gap extension penalty: 3.

Figure 2 shows the comparative amino acid alignments of vatD with four virginiamycin A acetyl transferase proteins. The satB protein is from *Enterococcus*, and vat, vatB, and vatC are from *Staphylococcus*.

Novel polynucleotides corresponding to the vatD gene from various strains of *Enterococcus faecium* have been isolated [and<sup>and</sup> sequenced. These polynucleotides include SEQ ID NO:2. By "polynucleotides" according to the invention is meant the sequence referred to as SEQ ID NO:2, and the complementary sequences and/or the sequences of polynucleotides that hybridize to the referred sequences in high stringent conditions (hybridization in a mixture containing 5 x SSPE, 5x Denhart solution, 0.5% SDS (w/v) and 100 µg/ml salmon sperm DNA]. The membrane on which is hybridized the DNA, is washed 2 times during 10 minutes, in 2x SSPE, 0.1% SDS (w/v) at room temperature and then the membrane (or the filter) is immersed in a solution of 1 x SSPE, 0.1% SDS (w/v) during 15 minutes at 68°C and finally in a

solution of 1 x SSPE, 0.1% SDS (w/v) during 15 minutes at 68°C. The polynucleotides according to the invention are used for detecting *Enterococcus faecium* strains carrying a gene encoding resistance to streptogramin A.

5 By "active molecule" according to the invention is meant a molecule capable of inhibiting the activity of the purified polypeptide as defined in the present invention or capable of inhibiting the bacterial culture of *Enterococcus faecium* strains.

10 Thus, the polynucleotides of SEQ ID NO:2 and its fragment can be used to select nucleotide primers notably for an amplification reaction, such as the amplification reactions further described. PCR is described in the U.S. Patent No. 4,683,202 granted to Cetus Corp. The  
15 amplified fragments may identified by agarose or polyacrylamide gel electrophoresis, or by a capillary electrophoresis, or alternatively by a chromatography technique (gel filtration, hydrophobic chromatography, or ion exchange chromatography). The specificity of the  
20 amplification can be ensured by a molecular hybridization using as nucleic probes the polynucleotides derived from SEQ ID NO:2 and its fragments, oligonucleotides that are complementary to these polynucleotides or fragments thereof, or their amplification products themselves.

25 Amplified nucleotide fragments are useful as probes in hybridization reactions in order to detect the presence of one polynucleotide according to the present invention or in order detect the presence of a bacteria of *Enterococcus faecium* strain carrying genes encoding resistance to streptogramin A, in a biological sample. This invention also provides, the amplified nucleic acid

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fragments ("amplicons") defined herein above. These probes and amplicons can be radioactively or non-radioactively labeled, using for example enzymes or fluorescent compounds.

5 Preferred nucleic acid fragments that can serve as primers according to the present invention are the following in the Fig. 1:

PRIMER F 5' -CAATATTGGAATTCGGGACTACACC-3' (SEQ ID NO:3)

EcoRI

10

nt 354

nt 378 gene [vatD] vate

PRIMER R 5' -CTGTTTATGAATTCAAGTGTGG-3' (SEQ ID NO:4)

EcoRI

nt 899

nt 878 gene [vatD] vate

15

The primers can also be used as oligonucleotide probes to specifically detect a polynucleotide according to the invention.

20

Other techniques related to nucleic acid amplification can also be used and are generally preferred to the PCR technique. The Strand Displacement Amplification (SDA) technique (Walker et al., 1992) is an isothermal amplification technique based on the ability of a restriction enzyme to cleave one of the strands at a recognition site (which is under a hemiphosphorothioate form), and on the property of a DNA polymerase to initiate the synthesis of a new strand from the 3' OH end generated by the restriction enzyme and on the property of this DNA polymerase to displace the previously synthesized strand being localized downstream.

25

The SDA amplification technique is more easily performed than PCR (a single thermostated water bath device is necessary and is faster than the other

amplification methods. Thus, the present invention also comprises using the nucleic acid fragment according to the invention (primers) in a method of DNA or RNA amplification according to the SDA technique. The polynucleotides of SEQ ID NO:2 and its fragments, especially the primers according to the invention, are useful as technical means for performing different target nucleic acid amplification methods such as:

- TAS (Transcription-based Amplification System), described by Kwoh et al. in 1989;
- SR (Self-Sustained Sequence Replication), described by Guatelli et al. in 1990;
- NASBA (Nucleic acid Sequence Based Amplification), described by Kievitis et al. in 1991; and
- TMA (Transcription Mediated Amplification).

The polynucleotides of SEQ ID NO:2 and its fragments, especially the primers according to the invention, are also useful as technical means for performing methods for amplification or modification of a nucleic acid used as a probe, such as:

- LCR (Ligase Chain Reaction), described by Landegren et al. in 1988 and improved by Barany et al. in 1991, who employ a thermostable ligase;
- RCR (Repair Chain Reaction), described by Segev et al. 1992;
- CPR (Cycling Probe Reaction), described by Duck et al. in 1990; and
- Q-beta replicase reaction, described by Miele et al. in 1983 and improved by Chu et al. in 1986, Lizardi et al. in 1988 and by Burg et al. and Stone et al. in 1996.

When the target polynucleotide to be detected is RNA, for example mRNA, a reverse transcriptase enzyme can be used before the amplification reaction in order to obtain a cDNA from the RNA contained in the biological sample. The generated cDNA can be subsequently used as the nucleic acid target for the primers or the probes used in an amplification process or a detection process according to the present invention.

Nucleic probes according to the present invention are specific to detect a polynucleotide of the invention. By "specific probes" according to the invention is meant any oligonucleotide that hybridizes with the polynucleotide of SEQ ID NO:2, and which does not hybridize with unrelated sequences. Preferred oligonucleotide probes according to the invention are SEQ ID NOS:5, 6, 7, or 8 or SEQ ID NOS:3 or 4.

In a specific embodiment, the purified polynucleotides according to the present invention encompass polynucleotides having at least 80% identity in their nucleic acid sequences with polynucleotide of SEQ ID NO:2. By percentage of nucleotide homology according to the present invention is intended a percentage of identity between the corresponding bases of two homologous polynucleotides, this percentage of identity being purely statistical and the differences between two homologous polynucleotides being located at random and on the whole length of said polynucleotides. The calculation was made according to the software GCG and the program "gap."

The oligonucleotide probes according to the present invention hybridize specifically with a DNA or RNA

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molecule comprising all or part of the polynucleotide of SEQ ID NO:2 under stringent conditions. As an illustrative embodiment, the stringent hybridization conditions used in order to specifically detect a polynucleotide according to the present invention are advantageously the following:

Prehybridization and hybridization are performed at 68°C a mixture containing:

- 5X SSPE (1X SSPE is .3 M NaCl, 30 mM tri-sodium citrate
- 5X Denhardt's solution
- 0.5% (w/v) sodium dodecyl sulfate (SDS); and
- 100 µg ml<sup>-1</sup> salmon sperm DNA

The washings are performed as follows:

- Two washings at laboratory temperature for 10 min. in the presence of 2 x SSPE and 0.1 % SDS;
- One washing at 68°C for 15 min. in the presence of 1 x SSPE, .1% SDS; and
- One washing at 68°C for 15 min. in the presence of 0.1 x SSPE and 0.1 % SDS.

The non-labeled polynucleotides or oligonucleotides of the invention can be directly used as probes. Nevertheless, the polynucleotides or oligonucleotides are generally labeled with radioactive element (<sup>32</sup>P, <sup>35</sup>S, <sup>3</sup>H, <sup>125</sup>I ) or by a non-isotopic molecule (for example, biotin, acetylaminofluorene, digoxigenin, 5-bromodesoxyuridin, fluorescein) in order to generate probes that are useful for numerous applications. Examples of non-radioactive labeling of nucleic acid fragments are described in the French Patent No. FR 78 10975 or by Urdea et al. or Sanchez Pescador et al. 1988.

Other labeling techniques can also be used, such as those described in the French patents 2 422 956 and 2 518 755. The hybridization step may be performed in different ways (Matthews et al. 1988). A general method comprises immobilizing the nucleic acid that has been extracted from the biological sample on a substrate (nitrocellulose, nylon, polystyrene) and then incubating, in defined conditions, the target nucleic acid with the probe. Subsequent to the hybridization step, the excess amount of the specific probe is discarded, and the hybrid molecules formed are detected by an appropriate method (radioactivity, fluorescence, or enzyme activity measurement).

Advantageously, the probes according to the present invention can have structural characteristics such that they allow signal amplification, such structural characteristics being, for example, branched DNA probes as those described by Urdea et al. in 1991 or in the European Patent No. 0 225 807 (Chiron).

In another advantageous embodiment of the present invention, the probes described herein can be used as "capture probes", and are for this purpose immobilized on a substrate in order to capture the target nucleic acid contained in a biological sample. The captured target nucleic acid is subsequently detected with a second probe, which recognizes a sequence of the target nucleic acid that is different from the sequence recognized by the capture probe.

The oligonucleotide fragments useful as probes or primers according to the present invention can be prepared by cleavage of the polynucleotide of SEQ ID NO:2

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by restriction enzymes, as described in Sambrook et al. in 1989. Another appropriate preparation process of the nucleic acids of the invention containing at most 200 nucleotides (or 200 bp if these molecules are double-stranded) comprises the following steps:

- synthesizing DNA using the automated method of beta-cyanethylphosphoramidite described in 1986;
- cloning the thus obtained nucleic acids in an appropriate vector; and
- purifying the nucleic acid by hybridizing to an appropriate probe according to the present invention.

A chemical method for producing the nucleic acids according to the invention, which have a length of more than 200 nucleotides (or 200 bp if these molecules are double-stranded) comprises the following steps:

- Assembling the chemically synthesized oligonucleotides having different restriction sites at each end;
- cloning the thus obtained nucleic acids in an appropriate vector; and
- purifying the nucleic acid by hybridizing to an appropriate probe according to the present invention.

The oligonucleotide probes according to the present invention can also be used in a detection device comprising a matrix library of probes immobilized on a substrate, the sequence of each probe of a given length being localized in a shift of or several bases, one from the other, each probe of the matrix library thus being complementary to a distinct sequence of the target



nucleic acid. Optionally, the substrate of the matrix can be a material able to act as an electron donor, the detection of the matrix positions in which hybridization has occurred being subsequently determined by an electronic device. Such matrix libraries of probes and methods of specific detection of a target nucleic acid are described in the European patent application No. 713 016, or PCT Application No. WO 95 33846, or also PCT Application No. WO 95 11995 (Affymax Technologies), PCT Application No. WO 97 02357 (Affymetrix Inc.), and also in U.S Patent No. 5,202,231 (Drmanac), said patents and patent iapplications being herein incorporated by reference.

The present invention also pertains to a family of recombinant plasmids containing at least a nucleic acid according to the invention. According to an advantageous embodiment, a recombinant plasmid comprises a polynucleotide of SEQ ID NO:2 or nucleic acid fragment thereof. More specifically, the following plasmid is part of the invention: pIP1801 or its fragments. Said fragments are derived from the use of restriction enzymes according to the restriction map of the gene [vatD], <sup>vafE</sup>as shown in Figure 3.

The present invention is also directed to the full length coding sequences of the [vatD] <sup>vafE</sup>gene from *Enterococcus faecium* available using the purified polynucleotides according to the present invention, as well as to the polypeptide enzymes encoded by these full length coding sequences. In a specific embodiment of the present invention, the full length coding sequence of the [vatD] <sup>vafE</sup>gene is isolated from a plasmid or cosmid library of

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the genome of *Enterococcus faecium* that has been screened with the oligonucleotide probe according to the present invention. The selected positive plasmid or cosmid clones hybridizing with the oligonucleotide probes of the invention are then sequenced in order to characterize the corresponding full length coding sequence, and the DNA insert of interest is then cloned in an expression vector conferring resistance to streptogramin A and related compounds.

A suitable vector for the expression in bacteria and in particular in *E. coli*, is the pQE-30 vector (QIAexpress) that allows the production of a recombinant protein containing a 6xHis affinity tag. The 6xHis tag is placed at the C-terminus of the recombinant polypeptide ATP binding motif conferring resistance to streptogramin A and related compounds.

The polypeptides according to the invention can also be prepared by conventional methods of chemical synthesis, either in a homogenous solution or in solid phase. As an illustrative embodiment of such chemical polypeptide synthesis techniques the homogenous solution technique described by Houbenweyl in 1974 may be cited.

The polypeptide conferring resistance to streptogramin A and related compounds is useful for the preparation of polyclonal or monoclonal antibodies that recognize the polypeptides or fragments thereof. The monoclonal antibodies can be prepared from hybridomas according to the technique described by Kohler and Milstein in 1975. The polyclonal antibodies can be prepared by immunization of a mammal, especially a mouse or a rabbit, with a polypeptide according to the

invention that is combined with an adjuvant, and then by purifying specific antibodies contained in the serum of the immunized animal on a affinity chromatography column on which has previously been immobilized the polypeptide that has been used as the antigen.

Consequently, the invention is also directed to a method detecting specifically the presence of a polypeptide according to the invention in a biological sample. The method comprises:

- a) bringing into contact the biological sample with an antibody according to the invention; and
- b) detecting antigen-antibody complex formed.

Also part of the invention is a diagnostic kit for *in vitro* detecting the presence of a polypeptide according to the present invention in a biological sample. The kit comprises:

- a polyclonal or monoclonal antibody as described above, optionally labeled; and
- a reagent allowing the detection of the antigen-antibody complexes formed, wherein the reagent carries optionally a label, or being able to be recognized itself by a labeled reagent, more particularly in the case when the above-mentioned monoclonal or polyclonal antibody is not labeled by itself.

Indeed, the monoclonal or polyclonal antibodies according to the present invention are useful as detection means in order to identify or characterize a *Staphylococcal* strain carrying gene encoding resistance to streptogramin A.

The invention also pertains to:

- A purified polypeptide or a peptide fragment having at least 10 amino acids, which is recognized by antibodies directed against a polynucleotide sequence conferring resistance to streptogramin and related compounds, corresponding to a polynucleotide sequence according to the invention.

- A polynucleotide comprising the full length coding sequence of a *Enterococcus faecium* streptogramin A resistant gene containing a polynucleotide sequence according to the invention.

- A monoclonal or polyclonal antibody directed against a polypeptide or a peptide fragment encoded by the polynucleotide sequences according to the invention.

- A method of detecting the presence of bacterium harboring the polynucleotide sequences according to the invention in a biological sample comprising:

a) contacting bacterial DNA of the biological sample with a primer or a probe according to the invention, which hybridizes with a nucleotide sequence encoding resistance to streptogramins;

b) amplifying the nucleotide sequence using said primer or said probe; and

c) detecting the hybridized complex formed between said primer or probe with the DNA.

A kit for detecting the presence of bacterium having resistance to streptogramin A and harboring the polynucleotide sequences according to the invention in a biological sample, said kit comprising:

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a) a polynucleotide probe according to the invention; and

b) reagents necessary to perform a nucleic acid hybridization reaction.

5 A kit for detecting the presence of bacterium having resistance to streptogramin A and harboring the polynucleotide sequences according to the invention in a biological sample, said kit comprising:

10 a) a polynucleotide probe according to the invention; and

b) reagents necessary to perform a nucleic acid hybridization reaction.

15 A method of screening active antibiotics for the treatment of the infections due to Gram-positive bacteria, comprising the steps of:

a) bringing into contact a Gram-positive bacteria having a resistance to streptogramin A and related compounds and containing the polynucleotide sequences according to the invention with the antibiotic; and

20 b) measuring an activity of the antibiotic on the bacteria having a resistance to streptogramins and related compounds.

25 A method of screening for active synthetic molecules capable of penetrating into a bacteria of the family of enterococcus, wherein the inhibiting activity of these molecules is tested on at least a polypeptide encoded by the polynucleotide sequences according to the invention comprising the steps of:

a) contacting a sample of said active molecules with the bacteria;

- b) testing the capacity of the active molecules to penetrate into the bacteria and the capacity of inhibiting a bacterial culture at various concentration of the molecules; and
- 5 c) choosing the active molecule that provides an inhibitory effect of at least 80% on the bacterial culture compared to an untreated culture.

10 An *in vitro* method of screening for active molecules capable of inhibiting a polypeptide encoded by the polynucleotide sequences according to the invention, wherein the inhibiting activity of these molecules is tested on at least said polypeptide, said method comprising the steps of:

- 15 a) extracting a purified polypeptide according to the invention;
- b) contacting the active molecules with said purified polypeptide;
- c) testing the capacity of the active
- 20 molecules, at various concentrations, to inhibit the activity of the purified polypeptide; and
- d) choosing the active molecule that provides an inhibitory effect of at least 80 % on the
- 25 activity of the said purified polypeptide.

In the inactivation by the O-acetylation of virginiamycin A mediated by [vatD], <sup>vat E</sup> the donor of acetyl group is probably acetyl coenzyme A. The acetylation reduced coenzyme A can react with 5<sup>5'</sup>-dithio bis 2 nitrobenzoate (DTNB) to yield 5 thio 2 nitrobenzoate with a 1:1 stoichiometry. The 5 thio 2 nitrobenzoate is

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yellow and has a high extinction coefficient ( $E = 00136 \text{ mM}^{-1} \text{ cm}^{-1}$ ) at  $\lambda$  412 nm. Therefore, the measurement of its appearance can be recorded by a spectrophotometer with great sensitivity.

5 As examples there are disclosed hereinafter the detection of chloramphenicol acetyl transferase activity. Similar conditions may be used for the detection of virginiamycin A activity to yield 5-thio-2-nitrobenzoate with a 1:1 stoichiometry. The thio-2-nitrobenzoate is  
10 yellow and has a high extinction coefficient ( $00136 \text{ mM}^{-1} \text{ cm}^{-1}$ ) at  $\lambda$  412 nm. Therefore, the measurement of its appearance can be recorded spectrophotometrically with great sensitivity.

#### Materials

- 15 - Bacterial strain(s) to be tested.  
- Mueller-Hinton (MH) broth (Gram-negative bacteria) or brain heart infusion (BHI) broth (Gram-positive cocci)  
- 50 ml centrifuge tubes  
20 - Eppendorf tubes  
- Low speed centrifuge  
- Refrigerated bench centrifuge  
- Sonicator  
- Double beam recording spectrophotometer  
25 equipped with a water jacketed cuvette  
- Tris-Cl 1M (pH 6.0)  
- Tris-Cl 1M (pH 7.8)  
- Dithiothreitol (DTT) 0.01 M  
- TDDT buffer: Tris-Cl 50 mM (pH 7.8)

DTT 20  $\mu$ M

- Acetyl coenzyme A (CoASAc) 10 mM (PH 6.0) :  
dissolve 8.2 mg of CoASAc in 1 ml of 5 mM Tris-  
Cl (pH 6.0). This solution can be stored  
frozen for 1 year in aliquots (100  $\mu$ l).
- 5        - 5, 5'-dithiobis-2-nitrobenzoic acid (DTNB) 10  
mM (PH 7.8) : dissolve 20  $\mu$ g of DTNB in 0.5 ml  
of 1 M Tris-Cl (pH 7.8) and add 4.5 ml of  
distilled water. This solution should be make  
fresh each time.
- 10       - Reaction mixture: CoASAc (10 mM, pH 6.0):100 $\mu$ l  
DTNB (10 mM, PH 7.8) :500  $\mu$ l  
Tris-Cl (1 M, PH 7.8):920  $\mu$ l  
H<sub>2</sub>O up to 10 ml

This volume is sufficient for 15

15 reactions.

- Chloramphenicol (Cm) 10 mM (pH 7.8): dissolve  
3.2 mg of Cm in 1 ml of 100 mM Tris-Cl (pH  
7.8). heat 10 min in water bath at 100°C.  
Store at +4°C.

20 Protocol

Day 1

1. Inoculate separately 5 ml of MH broth with  
bacterial strains to be tested. Grow overnight at 37°C  
with moderate shaking.

25 Day 2

2. Inoculate separately 35 ml of MH broth with 1  
ml of each overnight culture. Grow at 37°C  
with moderate shaking until the OD<sub>600nm</sub> is 0.8.
3. Centrifuge the cells (8000 rpm, 10 min, 4°C).  
Discard the supernatant and wash the pellet in  
1 ml of TDDT buffer. Centrifuge again and



resuspend the pellet in 1 ml of the same buffer.

4. Sonicate the cells at 4°C with 5 x 30 s pulses with 30 s rest in between.
5. Centrifuge the samples in an Eppendorf centrifuge (15000 rpm, 10 min, 4°C) to remove cell debris.
6. Transfer supernatants (S20) to other Eppendorf tubes and keep on ice until assayed. If the CAT assay is not performed on the same day, freeze the samples at -20°C. The CAT activity can be retained frozen for at least one month.
7. Pour 600 µl of reaction mixture to reference cuvette and sample cuvettes equilibrated at 37°C in a double beam recording spectrophotometer. let stand 2 min ar adjust OD<sub>412nm</sub> to 0.
8. Add 20 µl of S20 to sample cuvettes, mix well, and record OD<sub>412nm</sub> for 1-2 min to determine the background CAT activity.
9. When a constant slope is obtained, add 10 µl of Cm to cuvettes, mix well and record the increase in absorbence (OD<sub>412nm</sub>) for about 5 min. If the CAT activity is too high, a more reliable measure of activity can be obtained by diluting the S20.
10. Measure the amount of protein in the S20.
11. Determine the slope (OD<sub>412nm</sub>/min) before and after adding Cm and then subtract the background slope from the sample slope. The CAT enzyme specific activity expressed in

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nmole/min/mg is  $\Delta OD_{412nm}/0.0136/\text{mg protein}$   
 [0.0136 being the extinction coefficient ( $\text{mM}^{-1}\text{cm}^{-1}$   $\lambda_{412nm}$ ) of 5-thio-2-nitrobenzoate].

**Notes**

- 5                   - Since the formation of 5-thio-2-nitrobenzoate is accompanied by the appearance of a yellow coloration, CAT activity can be qualitatively appreciated *de visu* in step 9.
- 10                  - The crude extracts (S20) obtained from certain bacterial genera contain high thioesterase activity that may mask that of CAT since it also catalyzes the formation of reduced coenzyme A. On the
- 15                   other hand, DTNB was reported to inhibit certain CTAs from Gram-negative bacteria. In both cases, partial purification of the enzyme or the use of an alternate
- 20                   procedure is necessary to overcome these problems. Different methods for convenient CAT assays based on labelled acetyl
- coenzyme A (or butyryl coenzyme A) for acyl donor are available.
- 25                  - Chloramphenicol analogs, such as 3'-desoxychloramphenicol, can be used to induce CAT expression in Gram-positive bacteria. This compound is not acetylated by CATs (free inducer) and has little effect on protein synthesis.
- Medium containing carbohydrates other than glucose may be used for the growth of

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Gram-negative bacteria to avoid catabolic repression.

If an active molecule for inhibiting the activity of the bacterial enzyme (acetyl transferase) is added to a culture medium containing the resistant strain, the acetyl co-enzyme A present in said medium is not degraded. If the molecule to be tested is not active on the resistant bacteria, the amount of acetyl co-enzyme A decreases.

A test for screening the inhibiting activity of a molecule, for example, a new antibiotic or a new antibacterial agent, can comprise the following steps:

- a) adding purified active acetyl transferase vatD in a solution containing virginiamycin A at various concentrations, acetyl co-enzyme A,
- b) adding the molecule to be tested at various concentrations,
- c) revealing the presence of acetyl co-enzyme A activity and quantifying said acetyl coenzyme A, if necessary, and
- d) comparing the quantification of acetyl coenzyme A with a control without the new molecule.

A composition of a polynucleotide sequence encoding resistance to streptogramins and related compounds, or inducing resistance in Gram-positive bacteria, wherein said composition comprises a nucleotide sequence corresponding to the resistance phenotype of the plasmid pIP1807 deposited with the C.N.C.M. under the Accession No. I-2247 on July 7, 1999.

A method of detecting the presence of bacterium harboring the polynucleotide sequences according to the

invention in a biological sample, said method comprising the steps of:

- a) contacting said sample with an antibody according to the invention that recognizes a polypeptide encoded by said polynucleotide sequences; and
- b) detecting said complex.

A diagnostic kit for *in vitro* detecting the presence of bacterium harboring the polynucleotide sequences according to invention in a biological sample, said kit comprising:

- a) a predetermined quantity of monoclonal or polyclonal antibodies according to the invention;
- b) reagents necessary to perform an immunological reaction between the antibodies and a polypeptide encoded by said polynucleotide sequences; and
- c) reagents necessary for detecting said complex between the antibodies and the polypeptide encoded by said polynucleotide sequences.

Plasmids containing the polynucleotides from *Enterococcus faecium*, which confer streptogramin A resistance have been inserted into vectors, which have been deposited at the Collection Nationale de Cultures de Microorganismes ("C.N.C.M.") Institut Pasteur, 28, rue du Docteur Roux, 75724 Paris Cedex 15 France on July 7, 1999, as follows:

Plasmid  
pIP1801

Accession No.  
I-2247

This invention will now be described in greater detail in the following Example.

Example

A collection of 51 *E. faecium* strains was studied for resistance to streptogramins. The strains were isolated from fecal samples from poultry (n = 22), pigs (n = 5), farmers (n = 19) and (sub)urban residents (n = 5) in the Netherlands (Table 1). *sata* was previously found in 19 strains and *vgb* in a single strain by PCR (14). The *E. faecium* strains were analyzed for nucleotide sequences hybridizing at high stringency (65°C) with the eight genes previously found in staphylococcal and enterococcal plasmids conferring resistance to the mixtures: *sata* (18), *vat* (9), *vatB* (3), *vatC* (6), *vga* (7) and *vgaB* (4) conferring resistance to A compounds and the two genes, *vgb* (8) and *vgbB*(6), encoding lactonases hydrolyzing B compounds. Nineteen of the strains carried *sata* and the combination of *vat* and *vgb* was detected in a single strain, KH6 (Table 1). These two latter genes are contiguous and in the same relative position as in the staphylococcal plasmids in which *vat-vgb* are carried by a DNA fragment originating from the *E. faecalis* plasmid, pAM $\beta$ 1 (5).

Table 1. Relevant characteristics of the 51 *E. faecium* strains isolated in the Netherlands.

Strain		Sg <sup>R</sup> genes	
designation	Origin (city)	Designation (1)	Size (in kb) of the hybridizing HindIII fragment (2)
4	pig (Weert)	[vatD] <u>vatE</u>	1.8
14	pig (Weert)	[vatD] <u>vatE</u>	1.8
17	pig (Weert)	satA	4.5*
18	pig (Weert)	satA	3.8*
19	pig (Weert)	satA	3.8*
K12	turkey	[vatD] <u>vatE</u>	6.0*
K13	turkey	[vatD] <u>vatE</u>	5.6*
K14	turkey	[vatD] <u>vatE</u>	6.0*
K15	turkey	[vatD] <u>vatE</u>	5.6*
K36	turkey	satA	6.0*
K40	turkey	[vatD] <u>vatE</u>	3.6*
KS30	turkey	[vatD] <u>vatE</u>	1.4
KS31	turkey	[vatD] <u>vatE</u>	1.4
KS33	turkey	[vatD] <u>vatE</u>	1.4
SK1	broiler	[vatD] <u>vatE</u>	3.2*
SK2	broiler	[vatD] <u>vatE</u>	3.2*
SK3	broiler	[vatD] <u>vatE</u>	> 10*
SK6	broiler	satA	7.0*
SK7	broiler	[vatD] <u>vatE</u>	5.6*
SK8	broiler	[vatD] <u>vatE</u>	5.6*
SK13	broiler	[vatD] <u>vatE</u>	3.2*

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Strain		Sg <sup>R</sup> genes	
designation	Origin (city)	Designation (1)	Size (in kb) of the hybridizing HindIII fragment (2)
SK19	broiler	[vatD] <u>vatE</u>	3.9*
PS17	broiler	[vatD] <u>vatE</u>	4.3*
PS22	broiler	satA	4.0*
PS26	broiler	[vatD] <u>vatE</u>	4.3*
PS35	broiler	[vatD] <u>vatE</u>	4.3*
PS42	broiler	[vatD] <u>vatE</u>	4.3*
KH2	turkey farmer	[vatD] <u>vatE</u>	5.6*
KH4	turkey farmer	satA	3.9*
KH5	turkey farmer	[vatD] <u>vatE</u>	7.3*
KH6	turkey farmer	[vatD] <u>vatE</u>	5.6*
		vat-vgb	8.9
KH7	turkey farmer	[vatD] <u>vatE</u>	2.5
KH15	turkey farmer	satA	2.3*
KH18	turkey farmer	[vatD] <u>vatE</u>	2.3
KH19	turkey farmer	[vatD] <u>vatE</u>	2.3
KH29	turkey farmer	[vatD] <u>vatE</u>	2.3*
KH36	turkey farmer	satA	3.9
KH39	turkey farmer	[vatD] <u>vatE</u>	2.9
LKH2	chicken farmer	satA	4.0*
LKH4	chicken farmer	satA	4.3*
SKH4	chicken farmer	[vatD] <u>vatE</u>	2.5*
SKH8	chicken farmer	satA	5.6*
SKH11	chicken farmer	[vatD] <u>vatE</u>	2.5

Strain		Sg <sup>R</sup> genes	
designation	Origin (city)	Designation (1)	Size (in kb) of the hybridizing HindIII fragment (2)
SKH16	chicken farmer	satA	4.5*
SKH18	chicken farmer	satA	3.9*
SKH23	chicken farmer	satA	3.9*
M2	Suburban (Weert)	satA	3.9*
M5	suburban (Weert)	[vatD] <sup>vatE</sup>	1.9
R2	suburban (Roermond)	satA	3.9*
R24	suburban (Roermond)	satA	3.9*
W3	suburban (Weert)	satA	4.0*

(1) The strains were screened for Sg<sup>R</sup> genes by hybridization at high annealing temperature (65°C) (2) with probe consisting of (i) recombinant plasmids containing DNA inserts from within each of the following genes: vat(9), vatB (3), vatC (6), vga (7) or vgaB (4) or (ii) DNA fragments amplified from satA (18) or [vatD]<sup>vatE</sup> (this study) by PCR with the following pairs of primers: sat1 (nt position: 189-210 in satA, Acc. No. L12033) and sat2 (nt position: 760-782 in sat\_ or [vatD-F]<sup>vatE-F</sup> (nt position: 354-378 in [vatD]<sup>vatE</sup>, Acc. No. AF153312) and [vatD-R]<sup>vatE-R</sup> (nt position: 878-899 in [vatD]<sup>vatE</sup>).

(2) The HindIII fragments indicated with an asterisk were detected in extrachromosomal DNA bands (> 40 kb)



migrating above the chromosomal DNA fragments of the  
uncleaved total cellular DNA, in agarose gel  
electrophoresis in Tr- acetate buffer. In the other  
strains, the hybridizing bands comigrated with the  
5 chromosomal fragments, but the hybridization signals were  
as strong as those of the extrachromosomal DNA,  
suggesting that they may be carried plasmids.

Thirty-one of the tested *E. faecium* strains did not  
contain any of the eight genes investigated. PCR  
10 experiments were carried out at low annealing temperature  
(40°C) with a pair of degenerate primers, M and N (3,  
16), designed to amplify a DNA fragment from any sequence  
encoding a streptogramin A acetyltransferase containing  
two well conserved motifs, III and IV (3, 6, 16). A DNA  
15 fragment of the expected size (147 nt) was amplified from  
the cellular DNA of all the strains. The amplicon  
obtained with the strain K14 was sequenced using  
oligonucleotides M and N as primers. Its sequence was  
only 60.4 % to 68.6% similar to the SgA acetyltransferase  
20 genes (vat, vatB, vatC, satA), suggesting that the  
amplicon was from a different gene. A 5 kb *HindIII*  
fragment hybridizing with the sequenced amplicon was  
isolated from the cellular DNA of strain K14 and inserted  
into the *HindIII* site of pUC18. The resulting plasmid,  
25 pIP1798, was used to sequence 1080 nt of the insert  
including the sequences hybridizing with the 147 bp  
amplicon.

The sequence (registered in the GenBank EMBLdata  
Library under Accession No. AF153312) contains a 642 bp  
gene including an ATG start codon preceded, 6 nt  
upstream, by a putative ribosome-binding site. The free

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energy of association of the most stable structure between this site and the 3' terminus of the 16S rRNA was -61.5 kJ/mol. This gene, named [vatD]<sup>vatE</sup>, is similar to those encoding SgA acetyltransferases, sataA, vat, vatB, and vatC (54.3, 58.0, 60.0, and 60.1 % similarity, respectively).

[vatD]<sup>vatE</sup> encodes a putative 214 aa protein of 23,775 Da similar to xenobiotic acetyltransferases (17). It is most similar to the SgA acetyltransferases, SataA, Vat, VatB, and VatC (48.5, 50.0, 59.9 and 50.9 % identical amino acids, respectively).

Most vat-related genes in staphylococcal plasmids are contiguous to and downstream from another streptogramin-resistance (Sg<sup>R</sup>) gene. The pairs of genes are probably co-transcribed (12). However, analysis of the 270 and 170 nt sequences flanking [vatD]<sup>vatE</sup> did not suggest the presence of any contiguous Sg<sup>R</sup> gene.

A DNA fragment of 858 nt containing [vatD]<sup>vatE</sup> (nt 104 to nt 961, Accession No. AF153312) was amplified from pIP1798 and inserted between the EcoRI and SmaI sites of the shuttle vector, pOX7 (11). The resulting plasmid, pIP1801, introduced by electroporation in the *S. aureus* recipient, RN4220 (15), conferred resistance to pristinamycin IIA (MICs: 2 µg/ml for RN4220 [pOX7] and 8 µg/ml for RN4220 [pIP1801]).

The presence of [vatD]<sup>vatE</sup> in other strains was tested by hybridization experiments at high stringency. Nucleotide sequences hybridizing with [vatD]<sup>vatE</sup> probe were detected in the 32 strains which did not carry sataA, including the strain containing vat-vgb (Table 1). Total cellular DNA of strain KH6 was subjected to agarose gel electrophoresis. The [vatD]<sup>vatE</sup> and vat-vgb sequences migrated

to different positions, suggesting that they are not carried by the same plasmid.

The distribution of the streptogramin-resistance genes in the collection of *E. faecium* studied was clearly different from that found in staphylococci (2). It is worth checking whether the high prevalence of [*vatD*]<sup>*vatE*</sup> in this collection, is also observed among infectious clinical isolates.

\* \* \*

In summary, the present invention pertains to polynucleotides derived from *Enterococcus faecium* genes encoding resistance to streptogramin A and chemically related compounds. This invention also relates to the use of the polynucleotides as oligonucleotide primers or probes for detecting *Enterococcus faecium* strains that are resistant to streptogramin A and related compounds in a biological sample.

In another embodiment, the present invention is directed to the full length coding sequences of the *Enterococcus faecium* genes encoding for resistance to streptogramin A and to the polypeptides expressed by these full length coding sequences.

Further, this invention relates to the use of the expressed polypeptides to produce specific monoclonal or polyclonal antibodies that serve as detection means in order to characterize any *Enterococcus faecium* strain carrying genes encoding resistance to streptogramin A and chemically related compounds.

The present invention is also directed to diagnostic methods for detecting specific strains of *Enterococcus faecium* expected to be contained in a biological sample.

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The diagnostic methods use the oligonucleotide probes and primers as well as the antibodies of the invention raised against [vatD]<sup>vatE</sup> protein or its fragments.

5 The invention relates also to a method of screening of molecules, which are capable to inactivate the acetyl transferase activity in bacteria. A bacterial culture, which is resistant to virginiamycin A, can grow in the presence of virginiamycin, but cannot grow if a new molecule active against acetyl transferase activity is  
10 added to the culture medium.

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## SEQUENCE IDENTIFIERS

## SEQ ID NO:1

1 MTIPDANAIY HNSAIKEVVF IKNVIKSPNI EIGDYTTYDD PVNPTDFEKH  
51 VTHHYEFLGD KLIIGKFCSL ASGIEFIMNG ANHVMKGIST YPFNILGGDW  
5 101 QQYTPELTDL PLKGD TVVGN DVWFGQNVTV LPGVKIGDGA IIGANSVVTK  
151 DVAPYTIVGG NPIQLIGPRF EPEVIQALEN LAWWNKDIEW ITANVPKLMQ  
201 TTPTLELINS LME

## SEQ ID NO:2

10 ATGACTATAC CTGACGCAAA TGCAATCTAT CATAACTCAG CCATCAAAGA GGTGTCTTT  
ATCAAGAACG TGATCAAAAG TCCCAATATT GAAATTGGGG ACTACACCTA TTATGATGAC  
CCAGTAAATC CCACCGATTT TGAGAAACAC GTTACCCATC ACTATGAATT TCTAGGCGAC  
AAATTAATCA TCGGTAAATT TTGTTCTCTC GCCAGTGGCA TTGAATTTAT CATGAACGGT  
GCCAACCACG TAATGAAAGG TATTTGACT TATCCATTA ATATATTAGG TGGCGATTGG  
15 CAACAATACA CTCCTGAACT GACTGATTG CCGTTGAAAG GTGATACTGT AGTCGGAAAT  
GACGTGTGGT TTGGGCAAAA TGTGACCGTC CTACCAGGCG TAAAAATAGG TGACGGTGCC  
ATTATCGGAG CAAATAGTGT TGTAACAAAA GACGTCGCTC CATATACAAT TGTCGGTGCC  
AATCCAATTC AACTCATCGG ACCAAGATT GAACCGGAAG TTATTCAAGC ATTAGAAAAT  
CTGGCATGGT GGAATAAAGA TATTGAATGG ATAACGCTA ATGTTCTAA ACTAATGCAA  
ACAACACCCA CACTTGAATT GATAACAGT TTAATGGAAA AA

20 5'- CAATATTGGAATTCGGGACTACACC - 3' primer F SEQ ID NO:3  
EcoRI

5'- CTGTTTATGAATTCAGTGTGG - 3' primer R SEQ ID NO:4  
EcoRI

25 Seq. 4  
I M N G A N H SEQ ID NO:5

5'- ATH ATG AAY GCN AAY CAY - 3' primer M SEQ ID NO:6

G N D V W SEQ ID NO:7

5'- CCA NAC RTC RTT NCC - 3' primer N SEQ ID NO:8

(abbreviations: H=A,T,C Y=C,T N=A,C,T,G R=A,G)

PATENT  
Attorney Docket No. 03495-0193

A N A I Y H N S SEQ ID NO:9

5'- GCA AAT GCA ATC TAT CAT AAC TCA - 3' SEQ ID NO:10

M Q T T P T L E L SEQ ID NO:11

5'- ATG CAA ACA ACA CCC ACA CTT GAA TTG - 3' SEQ ID NO:12

5 5'- TAGAAAGAATTTCAGTGATTGTGG - 3' primer A SEQ ID NO:13  
EcoRI

5'- GGATTCACTAAATAGTAAAGGCCGTG - 3' primer B SEQ ID NO:14  
HaeIII

SEQ ID NO:15

10 AAATTTAGG CGCACAAAAA GAAAGAGTGT GACAAAACAT GGTTATGCTA CATGTTTAAG  
GTAAAAATAG TTATGTCACA ACTACTTATT TTTTACCCA ATCTTCTAGA CTATAATTAA  
AATTAAATAA CTCAATTCGG AGGTACTAAC CTGACTATAC CTGACGCAAA TGCAATCTAT  
CATAACTCAG CCATCAAAGA GGTTGACTTT ATCAAGAACG TGATCAAAAAG TCCCAATATT  
15 GAAATTGGGG ACTACACCTA TTATGATGAC CCAGTAAATC CCACCGATTT TGAGAAACAC  
GTTACCCATC ACTATGAATT TCTAGGCGAC AAATTAATCA TCGGTAAATT TTGTTCTCTC  
GCCAGTGGCA TTGAATTTAT CATGAACGGT GCCAACCACG TAATGAAAGG TATTTGACT  
TATCCATTTA ATATATTAGG TGGCGATTGG CAACAATACA CTCCTGAACT GACTGATTTG  
CCGTTGAAAG GTGATACTGT AGTCGGAAT GACGTGTGGT TTGGGCAAAA TGTGACCGTC  
20 CTACCAGGCG TAAAAATAGG TGACGGTGCC ATTATCGGAG CAAATAGTGT TGTAACAAAA  
GACGTCGCTC CATATACAAT TGTCGGTGGC AATCCAATTC AACTCATCGG ACCAAGATTT  
GAACCGGAAG TTATTCAAGC ATTAGAAAAT CTGGCATGGT GGAATAAAGA TATTGAATGG  
ATAACTGCTA ATGTTCTTAA ACTAATGCAA ACAACACCCA CACTTGAATT GATAAACAGT  
TTAATGGAAA AATAAAAACA AAAAAGCCGT GCAAGCAATC CAAAAATGAT TGTTTACACG  
G

WHAT IS CLAIMED IS:

1. A purified nucleic acid molecule comprising the DNA sequence of SEQ ID NO:2.

2. A purified nucleic acid molecule encoding an amino acid sequence comprising the sequence of SEQ ID NO:1.

3. A purified nucleic acid molecule that hybridizes to either strand of a denatured, double-stranded DNA comprising the nucleic acid sequence of any one of claims 1 or 2 under conditions of moderate stringency.

4. The purified nucleic acid molecule as claimed in claim 3, wherein said isolated nucleic acid molecule is derived by *in vitro* mutagenesis from SEQ ID NO:2 to NO 15.

5. A purified nucleic acid molecule degenerate from SEQ ID NOS:5, 6, 7, or 8 as a result of the genetic code.

6. A purified nucleic acid molecule, which encodes *vatD* polypeptide, an allelic variant of [*vatD*]<sup>*vatE*</sup> polypeptide DNA, or a homolog of [*vatD*]<sup>*vatE*</sup> polypeptide DNA.

7. A recombinant vector that directs the expression of a nucleic acid molecule selected from the group consisting of the purified nucleic acid molecules of claims 1, 2, 5, and 6.

8. A recombinant vector that directs the expression of a nucleic acid molecule of claim 3.

9. A recombinant vector that directs the expression of a nucleic acid molecule of claim 4.

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10. A purified polypeptide encoded by a nucleic acid molecule selected from the group consisting of the purified nucleic acid molecules of claims 1, 2, 5, and 6.

11. A purified polypeptide according to claim 10 having a molecular weight of approximately 23,775 kDa as determined by SDS-PAGE.

12. A purified polypeptide according to claim 10 in non-glycosylated form.

13. A purified polypeptide encoded by a nucleic acid molecule of claim 3.

14. A purified polypeptide according to claim 13 in non-glycosylated form.

15. A purified polypeptide encoded by a nucleic acid molecule of claim 4.

16. A purified polypeptide according to claim 15 in non-glycosylated form.

17. Purified antibodies that bind to a polypeptide of claim 10.

18. Purified antibodies according to claim 17, wherein the antibodies are monoclonal antibodies.

19. Purified antibodies that bind to a polypeptide of claim 13.

20. Purified antibodies according to claim 19, wherein the antibodies are monoclonal antibodies.

21. Purified antibodies that bind to a polypeptide of claim 15.

22. Purified antibodies according to claim 21, wherein the antibodies are monoclonal antibodies.

23. A host cell transfected or transduced with the vector of claim 7.

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24. A method for the production of  $[\text{vatD}]^{\text{vatE}}$  polypeptide comprising culturing a host cell of claim 23 under conditions promoting expression, and recovering the polypeptide from the culture medium.

25. The method of claim 24, wherein the host cell is selected from the group consisting of bacterial cells, yeast cells, plant cells, and animal cells.

26. A host cell transfected or transduced with the vector of claim 8.

27. A method for the production of  $[\text{vatD}]^{\text{vatE}}$  polypeptide comprising culturing a host cell of claim 26 under conditions promoting expression, and recovering the polypeptide from the culture medium.

28. The method of claim 27, wherein the host cell is selected from the group consisting of bacterial cells, yeast cells, plant cells, and animal cells.

29. A host cell transfected or transduced with the vector of claim 9.

30. A method for the production of  $[\text{vatD}]^{\text{vatE}}$  polypeptide comprising culturing a host cell of claim 29 under conditions promoting expression, and recovering the polypeptide from the culture medium.

31. The method of claim 30, wherein the host cell is selected from the group consisting of bacterial cells, yeast cells, plant cells, and animal cells.

32. The plasmid deposited at CNCM under the Accession Number I-2247.

33. An immunological complex comprising a  $[\text{vatD}]^{\text{vatE}}$  polypeptide and an antibody that specifically recognizes said polypeptide.

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34. A method of detecting a bacterium in a biological sample that harbors a polynucleotide sequence according to claim 1, said method comprising the steps of:

- a) contacting bacterial DNA of the biological sample with a primer or a probe according to claim 1 or 3 to 6, which hybridizes with a nucleotide sequence encoding resistance to streptogramins;
- b) amplifying the nucleotide sequence using said primer or said probe; and
- c) detecting a hybridized complex formed between said primer or probe and the DNA.

35. A kit for detecting a bacterium that is resistant to a streptogramin and harbors a polynucleotide sequence according to claim 1, said kit comprising:

- a) a polynucleotide probe according to claim 19 or 20; and
- b) reagents to perform a nucleic acid

hybridization reaction.

36. A kit for detecting a bacterium that is resistant to a streptogramin and harbors a polynucleotide sequence according to claim 2, said kit comprising:

- a) a polynucleotide probe according to claim 19 or 20; and
- b) reagents to perform a nucleic acid hybridization reaction.

37. A method of screening an active antibiotic for treating a Gram-positive bacterial infection, comprising the steps of:

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- a) contacting the antibiotic with Gram-positive bacteria that are resistant to a streptogramin and contain a polynucleotide sequence according to claim 1; and
- 5        b) determining the activity of the antibiotic on the bacteria.

38. A method of screening for active synthetic molecules capable of penetrating into a bacteria of the enterococcus family, wherein an inhibiting activity of the molecules is tested on at least a polypeptide encoded by a polynucleotide sequence according to claim 1, the method comprising the steps of:

10

- a) contacting a sample of said active molecules with the bacteria;
- 15        b) testing the capacity of the active molecules to penetrate into the bacteria and the capacity of inhibiting a bacterial culture at various concentration of the molecules; and
- c) choosing the active molecule that provides an inhibitory effect of at least 80% on the bacterial culture compared to an untreated culture.
- 20

39. An *in vitro* method of screening for active molecules capable of inhibiting a polypeptide encoded by a polynucleotide sequence according to claim 1, said method comprising the steps of:

25

- a) contacting the active molecules with said polypeptide;
- b) testing the capacity of the active molecules, at various concentrations, to inhibit the activity of the polypeptide; and

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- c) choosing the active molecule that provides an inhibitory effect of at least 80 % on the activity of the said polypeptide.

5 40. A method of detecting a bacterium in a biological sample that harbors a polynucleotide sequence according to claim 2, said method comprising the steps of:

- 10 a) contacting said sample with an antibody according to claim 17 that recognizes a polypeptide encoded by said polynucleotide sequences; and
- b) detecting a complex formed between the antibody and the polypeptide.

15 41. A diagnostic kit for *in vitro* detection of a bacterium harboring the polynucleotide sequences according to claim 2, said kit comprising:

- 20 a) a predetermined quantity of monoclonal or polyclonal antibodies according to claim 17;
- b) reagents to perform an immunological reaction between the antibodies and a polypeptide encoded by said polynucleotide sequences; and
- c) reagents for detecting a complex formed between the antibodies and the polypeptide encoded by said polynucleotide sequences.

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ABSTRACT

A gene encoding an acetyltransferase inactivating streptogramin A was isolated from an *Enterococcus faecium* strain and sequenced. The gene, designated [vatD],<sup>vat E</sup> encodes a 23,775 kDa protein exhibiting 48.5 to 59.9 % amino acid identity with four other enzymes with the same activity, Vat, VatB, VatC and SatA.

5